What is claimed is:

1. A method for enriching for target DNA sequences containing at least a partial coding region for at least one specified activity in a DNA sample comprising:
   a) co-encapsulating in a micro-environment a mixture of target DNA obtained from more than one organism with a mixture of DNA probes comprising a detectable marker and at least a portion of a DNA sequence encoding at least one enzyme having a specified enzyme activity;
   b) incubating the co-encapsulated mixture under such conditions and for such time as to allow hybridization of complementary sequences; and
   c) screening for the specified activity.

2. The method of claim 1, further comprising transforming host cells with recovered target DNA to produce an expression library of a plurality of clones.

3. The method of claim 1, wherein the organisms are microorganisms.

4. The method of claim 3, wherein the microorganisms are uncultured microorganisms.

5. The method of claim 1, further comprising screening the expression library for the specified enzyme activity.

6. The method of claim 1, wherein the target DNA obtained from the DNA population is selected by:

a) converting double stranded DNA into single stranded DNA;

b) recovering from the converted single stranded DNA, single stranded target DNA which hybridizes to probe DNA;

c) converting recovered single stranded target DNA to double stranded DNA; and

c) transforming a host cell with the double stranded DNA of c).

7. A method of FACS screening for an agent that modulates the activity of a target cell component, wherein the target cell component and a selectable marker are expressed by a eukaryotic cell, the method comprising co-encapsulating the agent in a microenvironment with the recombinant cell expressing the target cell component and detectable marker and detecting the effect of the agent on the activity of the cell component.

8. The method of claim 1, wherein said target DNA is gene cluster DNA.

9. The method of claim 4, wherein the uncultured microorganisms are derived from an environmental sample.

10. The method of claim 4, wherein the uncultured microorganisms comprise a mixture of terrestrial microorganisms or marine microorganisms or airborne microorganisms, or a mixture of terrestrial microorganisms, marine microorganisms and airborne microorganisms.

11. The method of claim 2, wherein the clones comprise a construct selected from the group consisting of phage, plasmids, phagemids, cosmids, fosmids, viral vectors, and artificial chromosomes.

12. The method of claim 1, wherein the target DNA comprises one or more operons, or portions thereof, of the DNA population.

13. The method of claim 12, wherein the operon or portions thereof encodes a complete or partial metabolic pathway.

14. The method of claim 4, wherein the uncultured microorganisms comprise extremophiles.

15. The method of claim 14, wherein the extremophiles are selected from the group consisting of thermophiles, hyperthermophiles, psychrophiles, barophiles, and psychrotrophs.

16. The method of claim 6, wherein the host cell is selected from the group consisting of a bacterium, fungus, plant cell, insect cell and animal cell.

17. The method of claim 1, wherein the target DNA encodes a protein.

18. The method of claim 17, wherein the protein is an enzyme.

19. The method of claim 18,wherein the enzyme is selected from the group consisting of oxidoreductases, transferases, hydrolases, lyases, isomerases, and ligases.

20. The method of claim 1, wherein the micro-environment is a liposome, gel microdrop, bead, agarose, cell, ghost red blood cell or ghost macrophage.

21. The method of claim 20, wherein the liposomes are prepared from one or more phospholipids, glycolipids, steroids, alkyl phosphates or fatty acid esters.

22. The method of claim 21, wherein the phospholipids are selected from the group consisting of lecithin, sphingomyelin and dipalmitoyl.

23. The method of claim 20, wherein the steroids are selected from the group consisting of cholesterol, cholestanol and lanosterol.

24. The method of claim 1, wherein the detectable marker is a fluorescent dye, a visible dye, a bioluminescent material, a chemiluminescent material, a radioactive material, or an enzymatic substrate.

25. The method of claim 24, wherein the bioluminescent material is green fluorescent protein (GFP) or red fluorescent protein (RFP).

26. The method of claim 25, wherein detection of the fluorescent dye or a visible dye is carried out by fluorometric or spectrophotometric measurement.